TABLE 1

Peptide sequence	HLA/MHC	MSTSD
untreated		7.5 1.1
RENLRIALRY	B2702	11.4 2.6 (1)*
YRLAIRLNER	-	12.1 2.8 (2)
renlrialry	-	11.4 4.1 (1)
yrlairlner	-	13.2 2.7 (2)
RVNLRIALRY	-	11.5 0.5 (3)
YRLAIRLNVR	-	12.5 1.6 (4)
rvnlrialry	-	13.1 3.9 (3)
yrlairlnvr	-	12.2 2.9 (4)
NLRIALRYYW	-	11.6 1.3 (5)
RVNLRTALRY	Kk	8.5 0.7 (6)
RVDLRTLLRY	Dk	7.0 0.5 (7)
RVDKRTLLGY	Kb	7.8 1.0 (8)
RVSLRNLLGY	Db	8.0 0.5 (9)
RESLRLLRGY	07	7.5 0.7 (10)
REDLRTLLRY	B2705	7.7 1.2 (11)
ENLRIALR	-	8.5 0.7 (12)
renlpialry	-	9.5 2.4 (13)
RVNLRTLRRY	E	8.0 0.5 (14)
RMNLQTLRGY	G	7.5 0.7 (15)

*Numbers in parentheses are SEQ ID NOS.

At page 33, lines 19-24, please replace the existing paragraph with the following:

Using the Combex program (Synt:em, Nímes, France), a combinatorial explosion was generated based on a consensus sequence RXXXRXXXY (SEQ ID NO: 16), derived from the learning set after aligning all active and inactive sequences. This sequence left seven positions, the positions represented by "X", to mutate in order to create the library.